Corresponding Author: David M. Dietz
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Manuscript Type: Brief Communication

# Main Figures: 3
# Supplementary Figures: 7
# Supplementary Tables: 2
# Supplementary Videos: n/a

Reporting Checklist for Nature Neuroscience

This checklist is used to ensure good reporting standards and to improve the reproducibility of published results. For more information, please read Reporting Life Sciences Research.

Please note that in the event of publication, it is mandatory that authors include all relevant methodological and statistical information in the manuscript.

### Statistics reporting, by figure

- Please specify the following information for each panel reporting quantitative data, and where each item is reported (section, e.g. Results, & paragraph number).
- Each figure legend should ideally contain an exact sample size (n) for each experimental group/condition, where n is an exact number and not a range, a clear definition of how n is defined (for example x cells from x slices from x animals from x litters, collected over x days), a description of the statistical test used, the results of the tests, any descriptive statistics and clearly defined error bars if applicable.
- For any experiments using custom statistics, please indicate the test used and stats obtained for each experiment.
- Each figure legend should include a statement of how many times the experiment shown was replicated in the lab; the details of sample collection should be sufficiently clear so that the replicability of the experiment is obvious to the reader.
- For experiments reported in the text but not in the figures, please use the paragraph number instead of the figure number.

Note: Mean and standard deviation are not appropriate on small samples, and plotting independent data points is usually more informative. When technical replicates are reported, error and significance measures reflect the experimental variability and not the variability of the biological process; it is misleading not to state this clearly.

<table>
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<tr>
<th>TEST USED</th>
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<th>DESCRIPITIVE STATS (AVERAGE, VARIANCE)</th>
<th>P VALUE</th>
<th>DEGREES OF FREEDOM &amp; F/T/Z/R/ETC VALUE</th>
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Nature Neuroscience: doi:10.1038/nn.4036
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<tr>
<td>Repeated Measures Two-Factor ANOVA; Tukey’s multiple comparison test</td>
<td>Online Methods: Statistical analyses Page 18</td>
<td>Cocaine 1 WD = 7 Saline 1 WD = 7 Cocaine 7 WD = 7 Saline 7 WD = 7</td>
<td>Heterogeneous Outbred non-litterate Male Sprague Dawley (Charles River) rats randomly assigned to cocaine/saline groups</td>
<td>Online Method: Regulation of Activin/Smad3 signaling following withdrawal from cocaine self-administration</td>
<td>Data expressed as mean +/- SEM</td>
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<tr>
<td>Two-Factor ANOVA; Tukey’s multiple comparison test</td>
<td>Online Methods: Statistical analyses Page 18</td>
<td>Cocaine 1 WD = 6 Saline 1 WD = 6 Cocaine 7 WD = 6 Saline 7 WD = 6</td>
<td>Heterogeneous Outbred non-litterate Male Sprague Dawley (Charles River) rats counterbalanced on SA performance before divided into withdrawal (1/7 WD) groups</td>
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<td>Data expressed as mean +/- SEM</td>
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<td>Two-Factor ANOVA; Tukey's multiple comparison test</td>
<td>Online Methods: Statistical analyses</td>
<td>Page 18</td>
<td>Cocaine 1WD = 5 Saline 1WD = 5 Cocaine 7WD = 6 Saline 7WD = 6</td>
<td>Heterogeneous Outbred non-littermate Male Sprague Dawley (Charles River) rats counterbalanced on SA performance before divided into withdrawal (1/7WD) groups</td>
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<td>Page 18</td>
<td>Cocaine 1WD = 5 Saline 1WD = 5 Cocaine 7WD = 6 Saline 7WD = 6</td>
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<tr>
<td>Repeated Measures Two-Factor ANOVA; Tukey’s multiple comparison test</td>
<td>Vehicle = 18 (Activin A Vehicle = 9; SB431542 Veh = 9)</td>
<td>Activin A = 7 SB43152 = 8</td>
<td>Heterogeneous Outbred Non-Littermate Male Sprague Dawley (Charles River) rats counterbalanced based on baseline within-session dose response performance before divided into microinjection groups.</td>
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<tr>
<td>Complete description of group allocation found in: Pharmacological manipulation of Activin-receptor signaling in the NAc. Cocaine dose response. Methods Page 12 - 13.</td>
<td>Data expressed as mean +/- SEM.</td>
<td>Interaction p = 0.0015.主效应: Dose p &lt; 0.001 Virus p &lt; 0.001. Follow-up: Dose 0.03: SB431542 vs vehicle = 0.9205 SB431542 vs Activin A = 0.5160 Activin A vs Veh = 0.3957 Dose 0.1: SB431542 vs vehicle = 0.0015 SB431542 vs Activin A = 0.0001 Activin A vs Veh = 0.0001 Dose 0.3: SB431542 vs vehicle = 0.0107 SB431542 vs Activin A = 0.0019 Activin A vs Veh = 0.0373 Dose 1.0: SB431542 vs vehicle = 0.1234 SB431542 vs Activin A = 0.0026 Activin A vs Veh = 0.0381</td>
<td>Interaction (dose x drug) F (6, 120) = 3.858 Main Effect (Dose) F(3,120) = 36.62 (Virus) F(2,120) = 17.00</td>
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<tr>
<td>Page</td>
<td>Online Methods: Statistical analyses</td>
<td>Page</td>
<td>Heterogeneous Outbred non-littermate Male Sprague Dawley (Charles River) rats counterbalanced on SA and extinction performance before divided into microinjection drug groups (Veh/SB431542)</td>
<td>Data expressed as mean +/- SEM</td>
<td>Fig. legend</td>
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<tr>
<td>13</td>
<td>Online Methods: Pharmacological manipulation of Activin-receptor signaling in the NAc Drug-induced reinstatement</td>
<td>13</td>
<td>Heterogeneous Outbred non-littermate Male Sprague Dawley (Charles River) rats counterbalanced on SA and extinction performance before divided into microinjection drug groups (Veh/Activin A)</td>
<td>Data expressed as mean +/- SEM</td>
<td>Fig. legend</td>
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<tr>
<td>13-14</td>
<td>Online Methods: Food reinforcement</td>
<td>13-14</td>
<td>Naive animals randomly assigned to groups</td>
<td>Data expressed as mean +/- SEM</td>
<td>Fig. legend</td>
</tr>
</tbody>
</table>
Repeated Measures Two-Factor ANOVA; Tukey’s multiple comparison test

Heterogeneous Outbred non-littermate Male Sprague Dawley (Charles River) rats counterbalanced based on baseline within-session dose response performance before divided into groups

Data expressed as mean +/- SEM

Interaction
P = 0.001
Main Effect:
Dose p < 0.001
Virus p < 0.001

Follow-up:
Dose 0.03: dnSmad3 vs GFP = 0.3974
dnSmad3 vs wtSmad3 = 0.1900
wtSmad3 vs GFP = 0.5209

Dose 0.1: dnSmad3 vs GFP = 0.0009
dnSmad3 vs wtSmad3 < 0.0001
wtSmad3 vs GFP = 0.0015

Dose 0.3: dnSmad3 vs GFP = 0.0320
dnSmad3 vs wtSmad3 = 0.0003
wtSmad3 vs GFP = 0.0124

Dose 1.0: dnSmad3 vs GFP = 0.5346
dnSmad3 vs wtSmad3 = 0.2510
wtSmad3 vs GFP = 0.5011

Fig. Legend
Interaction (dose x virus) F(6,144) = 5.007
Main Effect (Dose) F(3,144) = 32.57
(Virus) F(2,144) = 11.42

Online Methods: Alteration of Smad3 signaling in the NAc Cocaine dose-response Page 14-15

Online Methods: Data expressed as mean +/- SEM Page 14-15

Online Methods: Complete description of group allocaton found in:

Students t-test (unpaired)

Heterogeneous Outbred non-littermate Male Sprague Dawley (Charles River) rats counterbalanced on SA and extinction performance before divided into virus groups (GFP/dnSmad3)

Fig. Legend

Online Methods: Alteration of Smad3 signaling in the NAc Drug-induced reinstatement Page 15

p = 0.0139

Fig. Legend

Online Methods: Students t-test (unpaired) Page 18

Online Methods: Data expressed as mean +/- SEM Page 14-15

Online Methods: Statistical analyses Page 18
<p>| 2e (5mg /kg) viral drug reinstatement | Online Methods: Statistical analyses Page 18 | GFP = 11 wtSmad3 = 10 | Heterogeneous Outbred Male Sprague Dawley (Charles River) rats counterbalanced on SA and extinction performance before divided into virus groups (GFP/wtSmad3) | Fig. legend Online Methods: Alteration of Smad3 signaling in the NAc Drug-induced reinstatement Page 15 | Data expressed as mean +/- SEM | Fig. legend | p = 0.0479 | Fig. legend | t(19) = 2.115 | Fig. legend |
| 2f viral food rate responding | Online Methods: Statistical analyses Page 18 | GFP = 7 dnSmad3 = 7 wtSmad3 = 8 | Naive animals randomly assigned to groups | Online Methods: Food reinforcement Page 13-14 | Data expressed as mean +/- SEM | Fig. legend | p = 0.6447 | Fig. legend | F(2,19) = 0.4493 | Fig. legend |
| 3b dnSmad3 spine density | Online Methods: Statistical analyses Page 18 | Saline GFP = 5 Saline dnSmad3 = 4 Cocaine GFP = 4 Cocaine dnSmad3 = 4 | An average was obtained from 6 – 10 neurons per rat | Online Methods: Dendritic spine analysis Page 16-17 | Data expressed as mean +/- SEM | Fig. legend | Interaction P = 0.0003 Saline GFP vs Saline dnSmad3 = 0.0334 Saline GFP vs Cocaine GFP = 0.0002 Saline GFP vs Cocaine dnSmad3 = 0.7284 Saline dnSmad3 vs Cocaine GFP = 0.0234 Saline dnSmad3 vs Cocaine dnSmad3 = 0.0772 Cocaine GFP vs. Cocaine dnSmad3 = 0.0006 | Fig. legend | Interaction: F(1,13) = 23.92 | Fig. legend |</p>
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<th>3c</th>
<th>Online Methods: Statistical analyses</th>
<th>Page 18</th>
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</thead>
</table>
| +  | +  | Saline GFP = 4  
|    |    | Saline dnSmad3 = 4  
|    |    | Cocaine GFP = 4  
|    |    | Cocaine dnSmad3 = 4  
|    |    | 6-8 neurons/animal from 3-4 sections averaged per subject |
|    |    | Data expressed as mean +/- SEM |
|    |    | Interaction: p = 0.0074  
|    |    | Saline GFP vs Saline dnSmad3 = 0.0281  
|    |    | Saline GFP vs Cocaine GFP = 0.0009  
|    |    | Saline GFP vs Cocaine dnSmad3 = 0.0381  
|    |    | Saline dnSmad3 vs Cocaine dnSmad3 = 0.8711  
|    |    | Cocaine GFP vs. Cocaine dnSmad3 = 0.0624 |
|    |    | Fig. legend |

<table>
<thead>
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<th>Online Methods: Statistical analyses</th>
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</table>
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|    |    | Saline dnSmad3 = 4  
|    |    | Cocaine GFP = 4  
|    |    | Cocaine dnSmad3 = 4  
|    |    | 6-8 neurons/animal from 3-4 sections averaged per subject |
|    |    | Data expressed as mean +/- SEM |
|    |    | Main Effect (Drug) p = 0.0478  
|    |    | (Withdrawal) p = 0.0017  
|    |    | Saline GFP vs Saline dnSmad3 = 0.1875  
|    |    | Saline GFP vs Cocaine GFP = 0.9783  
|    |    | Saline GFP vs Cocaine dnSmad3 = 0.0010  
|    |    | Saline dnSmad3 vs Cocaine dnSmad3 = 0.1958  
|    |    | Saline dnSmad3 vs Cocaine dnSmad3 = 0.0124  
|    |    | Cocaine GFP vs. Cocaine dnSmad3 = 0.0010 |
|    |    | Main Effect (Drug) F (1,12) = 10.35  
<p>|    |    | (Withdrawal) F (1,12) = 16.28 |
|    |    | Fig. legend |</p>
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<td>Cocaine wtSmad3 = 5</td>
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<td>An average was obtained from 6–10 neurons per rat</td>
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<td>Main Effect: Drug &lt; 0.0001</td>
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<td>Virus = 0.0060</td>
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<td>Saline GFP vs Saline wtSmad3 = 0.2374</td>
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<td>Saline GFP vs Cocaine GFP = 0.0003</td>
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<th>3g  wtSmad3</th>
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<td>Two-Factor ANOVA; Tukey’s multiple comparison test</td>
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<td>Cocaine GFP = 4</td>
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<td>Cocaine wtSmad3 = 4</td>
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<td>6-8 neurons/animal from 3-4 sections averaged per subject</td>
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<td>Fig. legend</td>
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<td>Data expressed as mean +/- SEM</td>
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<td>Interaction &amp; Main Effects P &gt; 0.5</td>
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<td>Time</td>
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| 3h   | wtSmad3 | Two-Factor ANOVA; Tukey’s multiple comparison test | Saline GFP = 4
Saline wtSmad3 = 4
Cocaine GFP = 4
Cocaine wtSmad3 = 4 | 6-8 neurons/animal from 3-4 sections averaged per subject |Fig. legend |
|      | + mus |                    | Data expressed as mean +/- SEM |Fig. legend |
|      | - spine |                    | | |

**Cocaine GFP = 4**

**Cocaine wtSmad3 = 4**

**Saline GFP vs. Saline wtSmad3 = 0.0007**

**Saline GFP vs. Cocaine GFP = 0.0090**

**Saline GFP vs. Cocaine wtSmad3 < 0.0001**

**Saline wtSmad3 vs. Cocaine GFP = 0.1749**

**Saline wtSmad3 vs. Cocaine wtSmad3 = 0.1052**

**Cocaine GFP vs. Cocaine wtSmad3 = 0.0077**

---

**3i**

**PCR**

**One factor ANOVA; multiple comparison test**

**5-6 for saline and cocaine Ctnnb1 Grin2a Mef2d Cap2 Dbn1 Pdyn Cfl1**

**1 punch from each rat**

**Online Methods: Statistical analyses**

**Online Methods: Dendritic spine analysis**

**Data expressed as mean +/- SEM**

**Main Effect:**

**Main Effect (Drug)**

F(1,12) = 11.82

F(1,12) = 30.01

**Main Effect (Virus)**

**Main Effect (Virus)**

F(1,12) = 5.87

F(1,12) = 5.87

**Follow-up:**

0.0104 for Ctnnb1;
0.0131 for Grin2a;
0.0087 for Mef2d;
0.0129 for Cap2;
0.0003 for Dbn1;
0.0334 for Pdyn;
0.1053 for Cfl1

---

**3j**

**Smad3 chip**

**One factor ANOVA; multiple comparison test**

**5-7 for saline and cocaine Ctnnb1 Grin2a Mef2d Cap2 Dbn1 Pdyn Cfl1**

**7 punches from 2 rats equals one ChIP sample**

**Online Methods: Statistical analyses**

**Online Methods: Chromatin immunoprecipitation (ChIP) followed by qPCR**

**Data expressed as mean +/- SEM**

**Main Effect:**

**Main Effect (Drug)**

F(13,66)=5.523

**Main Effect (Virus)**

**Main Effect (Virus)**

F(13,66)=3.897

**Follow-up:**

0.0235 for Ctnnb1;
0.0026 for Grin2a;
0.0290 for Mef2d;
0.0045 for Cap2;
0.0205 for Dbn1;
0.4940 for Pdyn;
0.9986 for Cfl1

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### Table

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<th>Figure</th>
<th>Test</th>
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<tr>
<td><strong>Supp l. Fig 2a</strong></td>
<td>Students t-test (unpaired)</td>
<td>Heterogeneous Outbred non-littermate Male Sprague Dawley (Charles River) rats</td>
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<td>AcvR2a: cocaine (1 hr) = 5 saline (1 hr) = 6</td>
<td>Heterogeneous Outbred non-littermate Male Sprague Dawley (Charles River) rats</td>
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<td>Heterogeneous Outbred non-littermate Male Sprague Dawley (Charles River) rats</td>
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<td>Page 18</td>
<td>cocaine = 6 saline = 5</td>
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<td>Online Methods: Statistical analyses</td>
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<td>Online Methods: Statistical analyses</td>
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<td>Vehicle (DMSO) = 7 SB43154 2 = 7</td>
<td>Naive animals randomly assigned to groups</td>
<td>Supplementary Figure Legend</td>
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<td>Students t-test (unpaired)</td>
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<td>Naive animals randomly assigned to groups</td>
<td>Supplementary Figure Legend</td>
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</tbody>
</table>

**Online Methods:**

- **Statistical analyses:**
  - p = 0.59
  - p = 0.6544
  - p = 0.06
  - p = 0.02
  - p > 0.9999
  - p = 0.59

- **Supplementary Figure Legend:**
  - t(9) = 0.5546
  - t(9) = 0.4629
  - t(10) = 2.1
  - t(9) = 2.745
  - t(12) = 0.0
  - t(12) = 0.4833
### Representative figures

1. Are any representative images shown (including Western blots and immunohistochemistry/staining) in the paper?

   If so, what figure(s)?

   Yes.
   Figures 1c, 1d, 3a, 3e
   Suppl. Figure 5-7

2. For each representative image, is there a clear statement of how many times this experiment was successfully repeated and a discussion of any limitations in repeatability?

   If so, where is this reported (section, paragraph #)?

   Yes.
   Histology Figures (Supplemental 5b) showing localization of viral-mediated expression do not depend on repetitions, but rather are representations of the experiments conducted within the manuscript. The experiment was repeated independently at least two times (described in Online Methods: Dendritic Spine Analysis).

   Western Blotting: (Figures 1c, 1d, and Suppl. Fig 6-7) were repeated twice across 2 gels.
Statistics and general methods

1. Is there a justification of the sample size?
   If so, how was it justified?
   Where (section, paragraph #)?
   Even if no sample size calculation was performed, authors should report why the sample size is adequate to measure their effect size.

   No statistical methods were used to predetermine sample sizes, but our sample sizes are similar to those reported in previous works (Gancarz-Kausch et al., 2014; Gancarz-Kausch et al., 2013; Dietz et al., 2012) and based on expected effect sizes and power analyses. Further, as required by University at Buffalo's Institutional Animal Care and Use Committee, we use discretion in animal use. Will add statement of sample size justification in revised manuscript.

2. Are statistical tests justified as appropriate for every figure?
   Where (section, paragraph #)?
   a. If there is a section summarizing the statistical methods in the methods, is the statistical test for each experiment clearly defined?
   Yes.
   All statistical tests are described in detail in Online Methods: Statistical Analyses (Page 18)
   b. Do the data meet the assumptions of the specific statistical test you chose (e.g. normality for a parametric test)?
      Where is this described (section, paragraph #)?
      Yes. As part of statistical tests, Shapiro-Wilks test of normality were conducted. In events that normal distribution could not be assumed, non-parametric tests were utilized (now described in Online Methods: Statistical Analyses).
   c. Is there any estimate of variance within each group of data?
      Is the variance similar between groups that are being statistically compared?
      Where is this described (section, paragraph #)?
      Yes. Barlett’s Test of Homogeneity of variance was assessed (now described in Online Methods: Statistical Analyses, Page 18).
   d. Are tests specified as one- or two-sided?
   Yes, two-sided.
   e. Are there adjustments for multiple comparisons?
      Yes. Bonferroni Corrections/Tukey’s/Sidak Post Hoc corrections for multiple comparisons (described in Online Methods: Statistical Analyses).

3. Are criteria for excluding data points reported?
   Was this criterion established prior to data collection?
   Where is this described (section, paragraph #)?
   Yes.
   Only rats with patent catheters were used in data analyses of self-administration experiments (Online Methods: Jugular catheterization and patency testing; Page 10-11)
   The criterion for acquisition of cocaine self-administration was an average of ten infusions per day (Online Methods: Regulation of Activin/Smad3 signaling following withdrawal from cocaine self-administration; Page 8-9).
   Viral and cannula targeting to NAc shell was confirmed for all animals; Anything outside of this area were excluded for anatomically incorrect placements (Online Methods: Page 10 & 11).
   For rt-PCR and ChIP, if melt curve did not produce 1 distinct peak, samples were removed from analysis.
4. Define the method of randomization used to assign subjects (or samples) to the experimental groups and to collect and process data. If no randomization was used, state so. Where does this appear (section, paragraph #)?

Rats counterbalanced based on SA performance before divided into groups to control for history of drug intake (Online Methods: Regulation of Activin/Smad3 signaling following withdrawal from cocaine self-administration; Page 11-12)

5. Is a statement of the extent to which investigator knew the group allocation during the experiment and in assessing outcome included? If no blinding was done, state so. Where (section, paragraph #)?

Yes. All confocal acquisition and analyses of spines were conducted by investigators blind to the experimental conditions (Online Methods: Dendritic Spine Analyses; Page 16-17).

6. For experiments in live vertebrates, is a statement of compliance with ethical guidelines/regulations included? Where (section, paragraph #)?

Yes. This study was conducted in accordance with the guidelines set up by the Institutional Animal Care and Use Committee of the State University of New York at Buffalo (Online Methods: Subjects; Page 10)

7. Is the species of the animals used reported? Where (section, paragraph #)?

Yes. Naïve Male Sprague-Dawley rats (Online Methods: Subjects; Page 10)

8. Is the strain of the animals (including background strains of KO/transgenic animals used) reported? Where (section, paragraph #)?

Yes. Naïve Male Sprague-Dawley rats (275–350 g) (Online Methods: Subjects; Page 10)

9. Is the sex of the animals/subjects used reported? Where (section, paragraph #)?

Yes. Naïve Male Sprague-Dawley rats (275–350 g) (Online Methods: Subjects; Page 10)

10. Is the age of the animals/subjects reported? Where (section, paragraph #)?

n/a
Animals were approximately age-matched when purchased from Vendor (ordered based on weight: 250-275 g)

11. For animals housed in a vivarium, is the light/dark cycle reported? Where (section, paragraph #)?

Yes. Behavioral testing took place 7 d/wk during the dark phase of the 12 h light-dark cycle. (Online Methods: Subjects; Page 10)

12. For animals housed in a vivarium, is the housing group (i.e. number of animals per cage) reported? Where (section, paragraph #)?

Yes. Singly housed following surgery and for the duration of the self-administration phase of the experiments in order to protect the catheter/harness assembly. (Online Methods: Subjects; Page 10)

13. For behavioral experiments, is the time of day reported (e.g. light or dark cycle)? Where (section, paragraph #)?

Yes. Behavioral testing took place 7 d/wk during the dark phase of the 12 h light-dark cycle. (Online Methods: Subjects; Page 10)

14. Is the previous history of the animals/subjects (e.g. prior drug administration, surgery, behavioral testing) reported? Where (section, paragraph #)?

Yes. Naïve Male Sprague-Dawley rats (275–350 g) (Online Methods: Subjects; Page 10)
15. If any animals/subjects were excluded from analysis, is this reported?

Where (section, paragraph #)?

- Loss of patency, failure to acquire self-administration
- Viral and cannula targeting to NAc was confirmed for all animals;
Animals excluded for anatomically incorrect placements

a. How were the criteria for exclusion defined?

Where is this described (section, paragraph #)?

- Loss of patency, failure to acquire self-administration
- Viral and cannula targeting to NAc was confirmed for all animals;
Animals excluded for anatomically incorrect placements

b. Specify reasons for any discrepancy between the number of animals at the beginning and end of the study.

Where is this described (section, paragraph #)?

- Loss of patency, failure to acquire self-administration
- Viral and cannula targeting to NAc was confirmed for all animals;
Animals excluded for anatomically incorrect placements

Reagents

1. Have antibodies been validated for use in the system under study (assay and species)?

Yes.

a. Is antibody catalog number given?

Where does this appear (section, paragraph #)?

Yes. Online Methods, Western Blotting; Page 16

b. Where were the validation data reported (citation, supplementary information, Antibodypedia)?

Validation data were not reported in the submitted manuscript. The citations listed below are validation of the antibodies used in both Western Blotting and ChIP. These citations can be added to the revised manuscript.

Western Blotting:
- Smad3:

- pSmad3:

- AcvR2a:

ChIP:
- Smad3
2. If cell lines were used to reflect the properties of a particular tissue or disease state, is their source identified?

Where (section, paragraph #)?

a. Were they recently authenticated?

Where is this information reported (section, paragraph #)?

Data deposition

Data deposition in a public repository is mandatory for:

a. Protein, DNA and RNA sequences
b. Macromolecular structures
c. Crystallographic data for small molecules
d. Microarray data

Deposition is strongly recommended for many other datasets for which structured public repositories exist; more details on our data policy are available here. We encourage the provision of other source data in supplementary information or in unstructured repositories such as Figshare and Dryad.

We encourage publication of Data Descriptors (see Scientific Data) to maximize data reuse.

1. Are accession codes for deposit dates provided?

Where (section, paragraph #)?

Computer code/software

Any custom algorithm/software that is central to the methods must be supplied by the authors in a usable and readable form for readers at the time of publication. However, referees may ask for this information at any time during the review process.

1. Identify all custom software or scripts that were required to conduct the study and where in the procedures each was used.

2. If computer code was used to generate results that are central to the paper’s conclusions, include a statement in the Methods section under “Code availability” to indicate whether and how the code can be accessed. Include version information as necessary and any restrictions on availability.

Human subjects

1. Which IRB approved the protocol?

Where is this stated (section, paragraph #)?

2. Is demographic information on all subjects provided?

Where (section, paragraph #)?
3. Is the number of human subjects, their age and sex clearly defined?
   Where (section, paragraph #)?
   n/a

4. Are the inclusion and exclusion criteria (if any) clearly specified?
   Where (section, paragraph #)?
   n/a

5. How well were the groups matched?
   Where is this information described (section, paragraph #)?
   n/a

6. Is a statement included confirming that informed consent was obtained from all subjects?
   Where (section, paragraph #)?
   n/a

7. For publication of patient photos, is a statement included confirming that consent to publish was obtained?
   Where (section, paragraph #)?
   n/a

**fMRI studies**

For papers reporting functional imaging (fMRI) results please ensure that these minimal reporting guidelines are met and that all this information is clearly provided in the methods:

1. Were any subjects scanned but then rejected for the analysis after the data was collected?
   n/a

   a. If yes, is the number rejected and reasons for rejection described?
      Where (section, paragraph #)?
      n/a

2. Is the number of blocks, trials or experimental units per session and/or subjects specified?
   Where (section, paragraph #)?
   n/a

3. Is the length of each trial and interval between trials specified?
   n/a

4. Is a blocked, event-related, or mixed design being used? If applicable, please specify the block length or how the event-related or mixed design was optimized.
   n/a

5. Is the task design clearly described?
   Where (section, paragraph #)?
   n/a

6. How was behavioral performance measured?
   n/a

7. Is an ANOVA or factorial design being used?
   n/a
8. For data acquisition, is a whole brain scan used? If not, state area of acquisition.
   a. How was this region determined?

9. Is the field strength (in Tesla) of the MRI system stated?
   a. Is the pulse sequence type (gradient/spin echo, EPI/spiral) stated?
   b. Are the field-of-view, matrix size, slice thickness, and TE/TR/flip angle clearly stated?

10. Are the software and specific parameters (model/functions, smoothing kernel size if applicable, etc.) used for data processing and pre-processing clearly stated?

11. Is the coordinate space for the anatomical/functional imaging data clearly defined as subject/native space or standardized stereotaxic space, e.g., original Talairach, MNI305, ICBM152, etc? Where (section, paragraph #)?

12. If there was data normalization/standardization to a specific space template, are the type of transformation (linear vs. nonlinear) used and image types being transformed clearly described? Where (section, paragraph #)?

13. How were anatomical locations determined, e.g., via an automated labeling algorithm (AAL), standardized coordinate database (Talairach daemon), probabilistic atlases, etc.?

14. Were any additional regressors (behavioral covariates, motion etc) used?

15. Is the contrast construction clearly defined?

16. Is a mixed/random effects or fixed inference used?
   a. If fixed effects inference used, is this justified?

17. Were repeated measures used (multiple measurements per subject)?
   a. If so, are the method to account for within subject correlation and the assumptions made about variance clearly stated?

18. If the threshold used for inference and visualization in figures varies, is this clearly stated?

19. Are statistical inferences corrected for multiple comparisons?
a. If not, is this labeled as uncorrected?  

n/a

20. Are the results based on an ROI (region of interest) analysis?

a. If so, is the rationale clearly described?

n/a

b. How were the ROI’s defined (functional vs anatomical localization)?

n/a

21. Is there correction for multiple comparisons within each voxel?

n/a

22. For cluster-wise significance, is the cluster-defining threshold and the corrected significance level defined?

n/a

› Additional comments

Additional Comments